



SEQUENCE LISTING

<110> YAMASHITA, ICHIRO

<120> High estrogen-sensitive medaka fish

<130> 210217US-620-7249-0

<140> US 09/893,666

<141> 2001-06-29

<150> JP 2000-247729

<151> 2000-08-17

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<170> PatentIn version 3.1

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<213> Oryzias latipes

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<221> CDS

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ccagcactca gatccaggat cagcccagcc tcctcagagc tggagaccct ctccccacct 180

cgccctctcgc cccgtgaccc cctcggtgac atg tac cct gaa gag agc cgg ggt 234
Met Tyr Pro Glu Ser Arg Gly
1 5tct gga ggg gtg gct gtc gtg gac ttt ttg gaa ggg acg tac gac tat 282
Ser Gly Gly Val Ala Val Asp Phe Leu Glu Gly Thr Tyr Asp Tyr
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Ala Ala Pro Asn Pro Ala Thr Thr Pro Leu Tyr Ser Gln Ser Ser Thr
25 30 35 40ggc tac tac tct gct ccc ctg gaa aca aac gga ccc ccc tca gaa ggc 378
Gly Tyr Ser Ala Pro Leu Glu Thr Asn Gly Pro Pro Ser Glu Gly
45 50 55agt ctg cag tcc ctg ggc agt ggg ccg acg agc cct ctg gtg ttt gtg 426
Ser Leu Gln Ser Leu Gly Ser Gly Pro Thr Ser Pro Leu Val Phe Val
60 65 70

ccc tcc agc ccc aga ctc agt ccc ttt atg cat cca ccc agc cac cac 474

Pro Ser Ser Pro Arg Leu Ser Pro Phe Met His Pro Pro Ser His His			
75	80	85	
tat ctg gaa acc act tcc acg ccc gtt tac aga tcc agc cac cag gga			522
Tyr Leu Glu Thr Thr Ser Thr Pro Val Tyr Arg Ser Ser His Gln Gly			
90	95	100	
gcc tcc agg gag gac cag tgc ggc tcc cgg gag gac acg tgc agc ctg			570
Ala Ser Arg Glu Asp Gln Cys Gly Ser Arg Glu Asp Thr Cys Ser Leu			
105	110	115	120
ggg gag tta ggc gcc gga gcc ggg gct ggg ggg ttt gag atg gcc aaa			618
Gly Glu Leu Gly Ala Gly Ala Gly Gly Phe Glu Met Ala Lys			
125	130	135	
gac acg cgt ttc tgc gcc gtg tgc agc gac tac gcc tct ggg tac cac			666
Asp Thr Arg Phe Cys Ala Val Cys Ser Asp Tyr Ala Ser Gly Tyr His			
140	145	150	
tat ggg gtg tgg tct tgt gag ggc tgc aag gcc ttc ttc aag agg agc			714
Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser			
155	160	165	
atc cag ggt cac aat gac tat atg tgc cca gcg acc aat cag tgc act			762
Ile Gln Gly His Asn Asp Tyr Met Cys Pro Ala Thr Asn Gln Cys Thr			
170	175	180	
att gac aga aat cgg agg aag agc tgc cag gct tgt cgt ctt agg aag			810
Ile Asp Arg Asn Arg Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys			
185	190	195	200
tgt tac gaa gtg gga atg atg aaa ggc ggt gtg cgc aag gac cgc att			858
Cys Tyr Glu Val Gly Met Met Lys Gly Gly Val Arg Lys Asp Arg Ile			
205	210	215	
cgc att tta cgg cgt gac aaa cgg cgg aca ggc gtt ggt gat gga gac			906
Arg Ile Leu Arg Arg Asp Lys Arg Arg Thr Gly Val Gly Asp Gly Asp			
220	225	230	
aag gtt gta aag ggt cag gag cat aaa acg gtg cat tat gat gga agg			954
Lys Val Val Lys Gly Gln His Lys Thr Val His Tyr Asp Gly Arg			
235	240	245	
aaa cgc agc aca gga gga gga gga gga gga gga gga aga ctg			1002
Lys Arg Ser Ser Thr Gly Gly Gly Gly Gly Gly Gly Arg Leu			
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tct gtg acc agc ata cct cct gag cag gtg ctg ctc ctc ctt cag ggc			1050
Ser Val Thr Ser Ile Pro Pro Glu Gln Val Leu Leu Leu Gln Gly			
265	270	275	280
gcc gag ccc ccg ata ctc tgc tcg cgt cag aag ttg agc cga ccg tac			1098
Ala Glu Pro Pro Ile Leu Cys Ser Arg Gln Lys Leu Ser Arg Pro Tyr			
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acc gag gtc acc atg atg acc ctg ctc acc agc atg gca gac aag gag			1146
Thr Glu Val Thr Met Met Thr Leu Leu Thr Ser Met Ala Asp Lys Glu			

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305

310

ctg gtc cac atg atc gcc tgg gcc aag aag ctc cca ggt ttt ctg cag 1194
 Leu Val His Met Ile Ala Trp Ala Lys Lys Leu Pro Gly Phe Leu Gln
 315 320 325

ctg tcc ctg cac gat cag gtg ctg ctg gag agc tcg tgg ctg gag 1242
 Leu Ser Leu His Asp Gln Val Leu Leu Leu Glu Ser Ser Trp Leu Glu
 330 335 340

gtg ctc atg atc ggc ctc att tgg agg tcc atc cac tgt ccc ggg aag 1290
 Val Leu Met Ile Gly Leu Ile Trp Arg Ser Ile His Cys Pro Gly Lys
 345 350 355 360

ctc atc ttt gca caa gac ctc atc ctg gac agg aat gag gga gac tgc 1338
 Leu Ile Phe Ala Gln Asp Leu Ile Leu Asp Arg Asn Glu Gly Asp Cys
 365 370 375

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cgc ttc cgt gtg ctc aaa ctc aaa cct gag gaa ttc gtc tgc ctc aaa 1434
 Arg Phe Arg Val Leu Lys Leu Lys Pro Glu Glu Phe Val Cys Leu Lys
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gct att att tta ctc aac tcc ggt gct ttt tct ttc tgc acc ggc acc 1482
 Ala Ile Ile Leu Leu Asn Ser Gly Ala Phe Ser Phe Cys Thr Gly Thr
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atg gag cca ctt cac aac agc gcg gcg gtt cag agc atg ctg gac acc 1530
 Met Glu Pro Leu His Asn Ser Ala Ala Val Gln Ser Met Leu Asp Thr
 425 430 435 440

atc aca gac gca ctc att cat tac atc agt cag tcg ggt tac ttg gcc 1578
 Ile Thr Asp Ala Leu Ile His Tyr Ile Ser Gln Ser Gly Tyr Leu Ala
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cag gag cag gcg aga cgg cag gcc cag ctg ctc ctg ctg ctc tcc cac 1626
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atc agg cac atg agc aac aaa ggc atg gag cac ctc tac agc atg aag 1674
 Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met Lys
 475 480 485

tgc aag aac aaa gtc cct ctt tat gac ctc cta ctg gag atg ctc gat 1722
 Cys Lys Asn Lys Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu Asp
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 Val Asp Arg Asp Pro Pro Ser Thr Ser Ser Gly Gly Gly Gly Ile Ala
 525 530 535

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555 560 565	
tgc acc ccg gcc ctt caa gac tgagcacaca gtccaaggcc cttttttgt Cys Thr Pro Ala Leu Gln Asp	1965
570 575	
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35 40 45

Thr Asn Gly Pro Pro Ser Glu Gly Ser Leu Gln Ser Leu Gly Ser Gly
50 55 60

Pro Thr Ser Pro Leu Val Phe Val Pro Ser Ser Pro Arg Leu Ser Pro
65 70 75 80

Phe Met His Pro Pro Ser His His Tyr Leu Glu Thr Thr Ser Thr Pro
85 90 95

Val Tyr Arg Ser Ser His Gln Gly Ala Ser Arg Glu Asp Gln Cys Gly
100 105 110

Ser Arg Glu Asp Thr Cys Ser Leu Gly Glu Leu Gly Ala Gly Ala Gly
115 120 125

Ala Gly Gly Phe Glu Met Ala Lys Asp Thr Arg Phe Cys Ala Val Cys
130 135 140

Ser Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly
145 150 155 160

Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Met
165 170 175

Cys Pro Ala Thr Asn Gln Cys Thr Ile Asp Arg Asn Arg Arg Lys Ser
180 185 190

Cys Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu Val Gly Met Met Lys
195 200 205

Gly Gly Val Arg Lys Asp Arg Ile Arg Ile Leu Arg Arg Asp Lys Arg
210 215 220

Arg Thr Gly Val Gly Asp Gly Asp Lys Val Val Lys Gly Gln Glu His
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Lys Thr Val His Tyr Asp Gly Arg Lys Arg Ser Ser Thr Gly Gly Gly
245 250 255

Gly Gly Gly Gly Gly Arg Leu Ser Val Thr Ser Ile Pro Pro Glu

260

265

270

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Arg Gln Lys Leu Ser Arg Pro Tyr Thr Glu Val Thr Met Met Thr Leu
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305 310 315 320

Lys Lys Leu Pro Gly Phe Leu Gln Leu Ser Leu His Asp Gln Val Leu
325 330 335

Leu Leu Glu Ser Ser Trp Leu Glu Val Leu Met Ile Gly Leu Ile Trp
340 345 350

Arg Ser Ile His Cys Pro Gly Lys Leu Ile Phe Ala Gln Asp Leu Ile
355 360 365

Leu Asp Arg Asn Glu Gly Asp Cys Val Glu Gly Met Thr Glu Ile Phe
370 375 380

Asp Met Leu Leu Ala Thr Ala Ser Arg Phe Arg Val Leu Lys Leu Lys
385 390 395 400

Pro Glu Glu Phe Val Cys Leu Lys Ala Ile Ile Leu Leu Asn Ser Gly
405 410 415

Ala Phe Ser Phe Cys Thr Gly Thr Met Glu Pro Leu His Asn Ser Ala
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Ala Val Gln Ser Met Leu Asp Thr Ile Thr Asp Ala Leu Ile His Tyr
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Ile Ser Gln Ser Gly Tyr Leu Ala Gln Glu Gln Ala Arg Arg Gln Ala
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Gln Leu Leu Leu Leu Ser His Ile Arg His Met Ser Asn Lys Gly
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Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Lys Val Pro Leu Tyr
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Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His His Pro Val
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Arg Ala Pro Gln Ser Leu Ser Gln Val Asp Arg Asp Pro Pro Ser Thr
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Ser Ser Gly Gly Gly Ile Ala Pro Gly Ser Ile Ser Ala Ser Arg
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